



SEQUENCE LISTING

<110> Gately et al.

<120> PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
ANTIBODIES THERETO

<130> 1803-247

<140> 09/401,839

<141> 1999-09-22

<160> 34

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<212> PRT

<213> Homo sapiens

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Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln	Ser	Ser	Glu	Val	Leu	Gly	
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Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Gly	Asp	Ala	Gly	
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Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	Leu	Ser	His	Ser	Leu	Leu	
65				70						75					80	
Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Lys	
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Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Thr	Phe	Leu	Arg	Cys	Glu	Ala	Lys	
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Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Thr	Ile	Ser	Thr	
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Asp	Leu	Thr	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Ser	Ser	Asp	Pro	Gln	
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Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Gly	
145				150						155					160	
Asp	Asn	Lys	Glu	Tyr	Glu	Tyr	Ser	Val	Glu	Cys	Gln	Glu	Asp	Ser	Ala	
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Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Met	Val	Asp	Ala	
			180					185					190			
Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	Arg	
		195					200					205				
Asp	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln	Leu	Lys	Pro	Leu		
	210				215					220						
Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	Trp	
225				230						235					240	
Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Val	Gln	Val	Gln	
			245					250						255		
Gly	Lys	Ser	Lys	Arg	Glu	Lys	Lys	Asp	Arg	Val	Phe	Thr	Asp	Lys	Thr	
			260					265					270			

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
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 Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
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 Cys Ser
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 Met Cys His Gln Gln
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 Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu Ala Ser Pro Leu Val
 10 15 20

gcc ata tgg gaa ctg aag aaa gat gtt tat gtc gta gaa ttg gat tgg 151
 Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp
 25 30 35

tat ccg gat gcc cct gga gaa atg gtg gtc ctc acc tgt gac acc cct 199
 Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro
 40 45 50

gaa gaa gat ggt atc acc tgg acc ttg gac cag agc agt gag gtc tta 247
 Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu
 55 60 65

ggc tct ggc aaa acc ctg acc atc caa gtc aaa gag ttt gga gat gct 295
 Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala
 70 75 80 85

ggc cag tac acc tgt cac aaa gga ggc gag gtt cta agc cat tcg ctc 343
 Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu
 90 95 100

ctg ctg ctt cac aaa aag gaa gat gga att tgg tcc act gat att tta 391
 Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu
 105 110 115

aag gac cag aaa gaa ccc aaa aat aag acc ttt cta aga tgc gag gcc 439
 Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala
 120 125 130

aag aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg aca atc agt 487
 Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser
 135 140 145

act gat ttg aca ttc agt gtc aaa agc agc aga ggc tct tct gac ccc	535
Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro	
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caa ggg gtg acg tgc gga gct gct aca ctc tct gca gag aga gtc aga	583
Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg	
170 175 180	
ggg gac aaa caa gga tat gag tac tca gtg gag tgc cag gag gac agt	631
Gly Asp Lys Gln Gly Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser	
185 190 195	
gcc tgc cca gct gct gag gag agt ctg ccc att gag gtc atg gtg gat	679
Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp	
200 205 210	
gcc gtt cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc	727
Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile	
215 220 225	
agg gac atc atc aaa cct gac cca ccc aag aac ttg cag ctg aag cca	775
Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro	
230 235 240 245	
tta aag aat tct cgg cag gtg gag gtc agc tgg gag tac cct gac acc	823
Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr	
250 255 260	
tgg agt act cca cat tcc tac ttc tcc ctg aca ttc tgc gtt cag gtc	871
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val	
265 270 275	
cag ggc aag agc aag aga gaa aag aaa gat aga gtc ttc acg gac aag	919
Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys	
280 285 290	
acc tca gcc acg gtc atc tgc cgc aaa aat gcc agc att agc gtg cgg	967
Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg	
295 300 305	
gcc cag gac cgc tac tat agc tca tct tgg agc gaa tgg gca tct gtg	1015
Ala Gln Asp Arg Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val	
310 315 320 325	
ccc tgc agt taggttctga tccaggatga aaatttggag gaaaagtgga	1064
Pro Cys Ser	
agatattaag caaaatgttt aaagacacaa cggaatagac ccaaaaagat aatttctatc	1124
tgatttgctt taaaacgttt ttttaggatac acaatgatata ctttgctgta tttgtatagt	1184
tagatgctaa atgctcattg aaacaatcag ctaatttatg tatagatttt ccagctctca	1244
agttgccatg ggccttcacg ctatttaaata atttaagtaa tttatgtatt tattagtata	1304
ttactgttat ttaacgtttg tctgccagga tgtatggaat gtttcatact cttatgacct	1364
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			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
		35					40					45			
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln
	50					55					60				
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70					75					80
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	
Leu	Ser	His	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Thr	Phe
		115					120						125		
Leu	Arg	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp
	130					135					140				
Leu	Thr	Thr	Ile	Ser	Thr	Asp	Leu	Thr	Phe	Ser	Val	Lys	Ser	Ser	Arg
145					150					155					160
Gly	Ser	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser
				165					170					175	
Ala	Glu	Arg	Val	Arg	Gly	Asp	Lys	Gln	Gly	Tyr	Glu	Tyr	Ser	Val	Glu
			180					185						190	
Cys	Gln	Glu	Asp	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	Ile
		195					200						205		
Glu	Val	Met	Val	Asp	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr
	210					215					220				
Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn
225					230					235					240
Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser	Trp
				245					250					255	
Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr
			260					265					270		
Phe	Cys	Val	Gln	Val	Gln	Gly	Lys	Ser	Lys	Arg	Glu	Lys	Lys	Asp	Arg
		275					280						285		
Val	Phe	Thr	Asp	Lys	Thr	Ser	Ala	Thr	Val	Ile	Cys	Arg	Lys	Asn	Ala
	290					295					300				
Ser	Ile	Ser	Val	Arg	Ala	Gln	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser
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Met Cys Pro	
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gcg cgc agc ctc ctc ctt gtg gct acc ctg gtc ctc ctg gac cac ctc	226
Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu Asp His Leu	
5 10 15	
agt ttg gcc aga aac ctc ccc gtg gcc act cca gac cca gga atg ttc	274
Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe	
20 25 30 35	
cca tgc ctt cac cac tcc caa aac ctg ctg agg gcc gtc agc aac atg	322
Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met	
40 45 50	
ctc cag aag gcc aga caa act cta gaa ttt tac cct tgc act tct gaa	370
Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu	
55 60 65	
gag att gat cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag	418
Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu	
70 75 80	
gcc tgt tta cca ttg gaa tta acc aag aat gag agt tgc cta aat tcc	466
Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser	
85 90 95	
aga gag acc tct ttc ata act aat ggg agt tgc ctg gcc tcc aga aag	514
Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys	
100 105 110 115	
acc tct ttt atg atg gcc ctg tgc ctt agt agt att tat gaa gac ttg	562
Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu	
120 125 130	
aag atg tac cag gtg gag ttc aag acc atg aat gca aag ctt ctg atg	610
Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met	
135 140 145	
gat cct aag agg cag atc ttt cta gat caa aac atg ctg gca gtt att	658
Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile	
150 155 160	
gat gag ctg atg cag gcc ctg aat ttc aac agt gag act gtg cca caa	706
Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln	
165 170 175	
aaa tcc tcc ctt gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc	754
Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu	
180 185 190 195	
tgc ata ctt ctt cat gct ttc aga att cgg gca gtg act att gac aga	802
Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg	
200 205 210	

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 Val Thr Ser Tyr Leu Asn Ala Ser
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856

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 20 25 30
 Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
 35 40 45
 Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
 50 55 60
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
 65 70 75 80
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys
 85 90 95
 Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala
 100 105 110
 Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr
 115 120 125
 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys
 130 135 140
 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
 145 150 155 160
 Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr
 165 170 175
 Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
 180 185 190
 Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
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Pro Asp Ala Pro Gly Glu Met
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Asn Lys Thr Phe Leu Arg
 1           5

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 1 5

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 1 5 10

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<400> 13
 Ile Trp Glu Leu Lys Lys
 1 5

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<400> 14
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 1 5 10 15
 Pro

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<400> 20
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 1 5

<210> 21
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 <212> PRT
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<400> 21
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 1 5 10

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<210> 24
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